

OIEP

RAW SEQUENCE LISTING

DATE: 09/26/2000

PATENT APPLICATION: US/09/664,840

TIME: 12:02:24

Input Set : A:\BB1117 US NA Seq Listing.txt

Output Set: N:\CRF3\09262000\I664840.raw

ENTERED

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3 <110> APPLICANT: Cahoon, Edgar B.
4      Hitz, William D.
5      Kinney, Anthony J.
6      Vollmer, Steven J.
8 <120> TITLE OF INVENTION: LIMNANTHES OIL GENES
10 <130> FILE REFERENCE: BB1117 US NA
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/664,840
C--> 13 <141> CURRENT FILING DATE: 2000-09-19
15 <150> PRIOR APPLICATION NUMBER: 60/078,736
16 <151> PRIOR FILING DATE: 1998-03-20
18 <150> PRIOR APPLICATION NUMBER: PCT/US99/05471
19 <151> PRIOR FILING DATE: 1999-03-12
21 <160> NUMBER OF SEQ ID NOS: 7
23 <170> SOFTWARE: MICROSOFT OFFICE 97
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1355
27 <212> TYPE: DNA
28 <213> ORGANISM: Limnanthes douglasii
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32 tggcttcttt catcgcaacc acaacaccag caatgccagc ttctgcttca gttcttgatc 120
33 caaaaatacc cacaaaacca gaacccaaaa ccgaaacccc caaaccaaaa gacgatctcg 180
34 aacgcttcgc gacatcagaa gtcgtgttgg agaggaaatc caaaggattc tggcgccgga 240
35 aatggaaccc tcgtgatatt caaacgcgcg tcactttact ggtcctgcac gctcttgcag 300
36 cgatggcgcc cttttatttc agctgggatg cgttttggat ctcttttate ttgcttggtt 360
37 tcgcaagcgg tgttcttggg atcactttgt gcttccatag gtgtcttact catggcggtt 420
38 tcaagcttcc taagtgtggt gactacttct ttgcctactg tggctctctc gctcttcagg 480
39 gagatcccat ggaatgggtg agcaaccata ggtaccatca ccagttcgtc gatacagaaa 540
40 gagatgttca tagtccaact caaggatttt ggttctgtca cattggttgg gttcttgaca 600
41 aagatttatt cgtcgaaaaa cgtggtggcc gaagaaacaa tgtgaatgat ttgaagaaac 660
42 aagccttcta cagattcttc cagaaaactt atatgtacca tcaattggct ctaatagctc 720
43 tactttacta cgtcggaggg ttccataca ttgtctgggg aatgggtttt agattggtgt 780
44 ttatgttcca ttccacttcc gctatcaact cagtttgtca taaatggggc ggaaggccat 840
45 ggaatactgg agatttatcg accaacaata tgtttgttgc attgtgtgcg ttggagagg 900
46 gctggcataa caaccaccac gcattcgaac aatcagctcg acacgggcta gaatggtggc 960
47 agatcgatgt tacttggtac gttatcagga ctctacaagc tattggattg gctaccaatg 1020
48 tgaagctacc aactgaagct cagaagcaaa agctcaaaagc aaagagtgcg taaggagttt 1080
49 gaagcatgta ataagtgttt gtattcgata cctacttata tatgtttcta gactcgtaac 1140
50 tgtaatgaat aaagtccgag gcagctatat agactgtgtt cggatatgaa aatcggttga 1200
51 ttcttgtatc tgatcgaaaa tagctgcctt gatagggtgt cgataaaaca ttgttatggt 1260
52 gcttgggtga gttgtgtggg tcttgcttgg tactgtattg tgttgtgtca cgttttgaga 1320
53 ttatatatag tttcttgtg ttcaaaaaaa aaaaa 1355
55 <210> SEQ ID NO: 2
56 <211> LENGTH: 356
57 <212> TYPE: PRT
58 <213> ORGANISM: Limnanthes douglasii
60 <400> SEQUENCE: 2

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61 Leu Arg Leu Ser Leu Tyr Phe Pro Ile Ser Ile Ser Leu Ser Leu Ser
62 1 5 10 15
64 Leu Glu Ala Met Ala Ser Phe Ile Ala Thr Thr Thr Pro Ala Met Pro
65 20 25 30
67 Ala Phe Ala Ser Val Leu Asp Pro Lys Ile Pro Thr Lys Pro Glu Pro
68 35 40 45
70 Lys Thr Glu Thr Pro Lys Pro Lys Asp Asp Leu Glu Arg Phe Arg Thr
71 50 55 60
73 Ser Glu Val Val Leu Glu Arg Lys Ser Lys Gly Phe Trp Arg Arg Lys
74 65 70 75 80
76 Trp Asn Pro Arg Asp Ile Gln Asn Ala Val Thr Leu Leu Val Leu His
77 85 90 95
79 Ala Leu Ala Ala Met Ala Pro Phe Tyr Phe Ser Trp Asp Ala Phe Trp
80 100 105 110
82 Ile Ser Phe Ile Leu Leu Gly Phe Ala Ser Gly Val Leu Gly Ile Thr
83 115 120 125
85 Leu Cys Phe His Arg Cys Leu Thr His Gly Gly Phe Lys Leu Pro Lys
86 130 135 140
88 Leu Val Glu Tyr Phe Phe Ala Tyr Cys Gly Ser Leu Ala Leu Gln Gly
89 145 150 155 160
91 Asp Pro Met Glu Trp Val Ser Asn His Arg Tyr His His Gln Phe Val
92 165 170 175
94 Asp Thr Glu Arg Asp Val His Ser Pro Thr Gln Gly Phe Trp Phe Cys
95 180 185 190
97 His Ile Gly Trp Val Leu Asp Lys Asp Leu Phe Val Glu Lys Arg Gly
98 195 200 205
100 Gly Arg Arg Asn Asn Val Asn Asp Leu Lys Lys Gln Ala Phe Tyr Arg
101 210 215 220
103 Phe Leu Gln Lys Thr Tyr Met Tyr His Gln Leu Ala Leu Ile Ala Leu
104 225 230 235 240
106 Leu Tyr Tyr Val Gly Gly Phe Pro Tyr Ile Val Trp Gly Met Gly Phe
107 245 250 255
109 Arg Leu Val Phe Met Phe His Ser Thr Phe Ala Ile Asn Ser Val Cys
110 260 265 270
112 His Lys Trp Gly Gly Arg Pro Trp Asn Thr Gly Asp Leu Ser Thr Asn
113 275 280 285
115 Asn Met Phe Val Ala Leu Cys Ala Phe Gly Glu Gly Trp His Asn Asn
116 290 295 300
118 His His Ala Phe Glu Gln Ser Ala Arg His Gly Leu Glu Trp Trp Gln
119 305 310 315 320
121 Ile Asp Val Thr Trp Tyr Val Ile Arg Thr Leu Gln Ala Ile Gly Leu
122 325 330 335
124 Ala Thr Asn Val Lys Leu Pro Thr Glu Ala Gln Lys Gln Lys Leu Lys
125 340 345 350
127 Ala Lys Ser Ala
128 355
130 <210> SEQ ID NO: 3
131 <211> LENGTH: 305
132 <212> TYPE: PRT

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Input Set : A:\BB1117 US NA Seq Listing.txt
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133 <213> ORGANISM: Arabidopsis thaliana
135 <400> SEQUENCE: 3
136 Met Ser Leu Ser Ala Ser Glu Lys Glu Glu Asn Asn Lys Lys Met Ala
137 1 5 10 15
139 Ala Asp Lys Ala Glu Met Gly Arg Lys Lys Arg Ala Met Trp Glu Arg
140 20 25 30
142 Lys Trp Lys Arg Leu Asp Ile Val Lys Ala Phe Ala Ser Leu Phe Val
143 35 40 45
145 His Phe Leu Cys Leu Leu Ala Pro Phe Asn Phe Thr Trp Pro Ala Leu
146 50 55 60
148 Arg Val Ala Leu Ile Val Tyr Thr Val Gly Gly Leu Gly Ile Thr Val
149 65 70 75 80
151 Ser Tyr His Arg Asn Leu Ala His Arg Ser Phe Lys Val Pro Lys Trp
152 85 90 95
154 Leu Glu Tyr Phe Phe Ala Tyr Cys Gly Leu Leu Ala Ile Gln Gly Asp
155 100 105 110
157 Pro Ile Asp Trp Val Ser Thr His Arg Tyr His His Gln Phe Thr Asp
158 115 120 125
160 Ser Asp Arg Asp Pro His Ser Pro Asn Glu Gly Phe Trp Phe Ser His
161 130 135 140
163 Leu Leu Trp Leu Phe Asp Thr Gly Tyr Leu Val Glu Lys Cys Gly Arg
164 145 150 155 160
166 Arg Thr Asn Val Glu Asp Leu Lys Arg Gln Trp Tyr Tyr Lys Phe Leu
167 165 170 175
169 Gln Arg Thr Val Leu Tyr His Ile Leu Thr Phe Gly Phe Leu Leu Tyr
170 180 185 190
172 Tyr Phe Gly Gly Leu Ser Phe Leu Thr Trp Gly Met Gly Ile Gly Val
173 195 200 205
175 Ala Met Glu His His Val Thr Cys Leu Ile Asn Ser Leu Cys His Val
176 210 215 220
178 Trp Gly Ser Arg Thr Trp Lys Thr Asn Asp Thr Ser Arg Asn Val Trp
179 225 230 235 240
181 Trp Leu Ser Val Phe Ser Phe Gly Glu Ser Trp His Asn Asn His His
182 245 250 255
184 Ala Phe Glu Ser Ser Ala Arg Gln Gly Leu Glu Trp Trp Gln Ile Asp
185 260 265 270
187 Ile Ser Trp Tyr Ile Val Arg Phe Leu Glu Ile Ile Gly Leu Ala Thr
188 275 280 285
190 Asp Val Lys Leu Pro Ser Glu Ser Gln Arg Arg Arg Met Ala Met Val
191 290 295 300
193 Arg
194 305
196 <210> SEQ ID NO: 4
197 <211> LENGTH: 1807
198 <212> TYPE: DNA
199 <213> ORGANISM: Limnanthes douglasii
201 <220> FEATURE:
202 <221> NAME/KEY: unsure
203 <222> LOCATION: (302)..(303)

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205 <220> FEATURE:
206 <221> NAME/KEY: unsure
207 <222> LOCATION: (312) ✓
209 <220> FEATURE:
210 <221> NAME/KEY: unsure
211 <222> LOCATION: (315) ✓
213 <220> FEATURE:
214 <221> NAME/KEY: unsure
215 <222> LOCATION: (421) ✓
217 <220> FEATURE:
218 <221> NAME/KEY: unsure
219 <222> LOCATION: (1727) ✓
221 <400> SEQUENCE: 4
222 ctcaactctca cactctcttc tctctctttg tcggcttctc cggcgagata ctcaacggat 60
223 tcaatcgaag ggtagtacaa tatgtcggag acaaaacctg agaaaccttt gatcgcaacc 120
224 gtgaaaaaca cactacctga tttaaaacta tcaataaact taaaacacgt gaaactcggg 180
225 taccattacc tgatcaccca tggaaatgtac ctgtgtctcc ctctctctgc actagtccctc 240
226 ttgcgtcaaa tcgaactttt gtcctcctcaaa gatttcaacg acatctggga acagcttcag 300
W--> 227 ttnaatctca tntcngtcgt tggttcatca acacttcttg tctccttact taccctttac 360
228 tycatgactc gtcggaggcc ggtttatttg atggatttcg cgtgctataa acccgacgaa 420
W--> 229 nctcgaaaat ctactagaga acattttatg_aagtgtggtg_agagtgtggg...ctcttttaacg 480
230 gaggataata tcgattttca gaggaaatta gtcgcacgat ctggacttgg tgatgctacg 540
231 tattttacctg aagctatcgg tactatcccg gtcctatccg cgatgaaagc tgcgagaaga 600
232 gaagctgagt tggatgatgt tgggtgcgatt gatcaacttt tggagaagac aaaggtgaat 660
233 ccgaaggata tagggatctt ggttgtaaat tgcagcctgt ttagtccgac tccgtccctc 720
234 tcgtcgatga ttgtaacca ctataaaact cgtgggaaca ttataagcta caatctaggg 780
235 ggaatgggtt gcagtgcctg ttttaatttcg gtcgacttag ctaaaagact tctcgagaca 840
236 aatccaaaca cttacgcttt agttatgagc actgaaaata tcacactaaa ctggtacatg 900
237 ggcaatgacc ggtccaaact cgtgtccaat tgtcttttcc ggatgggagg agctgcggtc 960
238 ttgttatcaa acaaaacctc tgataagaaa agatcgaaat atcagttggt tactaccgtc 1020
239 cgaagccaca aaggtgctga cgataattgc tacggttgca tattccaaga agaagactcc 1080
240 aacggcaaaa tcggtgtaag cctctccaaa aatctaattg cggtcgcagg ggacgcgctt 1140
241 aagactaaca tcacgacgct tgggtccgtt gttttaccaa tgcggaaca acttttggtt 1200
242 ttcgccacgc tgggtgctgc aaaagttttc aagaagaaaa ttaagcccta cattccggac 1260
243 tttaaactag cttttgatca tttctgtatt catgcgggtg gtcgagctgt tttggacgag 1320
244 cttgagaaga atttgcaatt gtcaagctgg catctagagc cgtcgagaat gacgtttatc 1380
245 cggtttggtg atacgtcgag tagtactttg tggtagcagc tggcgtatcc ggaagccaaa 1440
246 gggaggatta gaaaaggaga aagagtttgg cagatagggt ttggttcttg gtttaaatgt 1500
247 aatagtgcgt tctggaaagc cttaaagagc gttgatccaa agaaagagaa caatccatgg 1560
248 atggatgaga tccaccagtt tccggttgcg gttgtctaa gttgtgtttt gatgtttaat 1620
249 gtttggtgtg ttgatgcttg ctaattgggt agtgtaagaa gtacttggtt gctgctggtt 1680
W--> 250 caattactaa ctaaagagag tgttgataaa gcatagaaca aagtaantaa ctggaagtg 1740
251 ctttgttgtt tgttcagtaa ctctattact gctgaatttc tctcaagaga agaattatgt 1800
252 ttaaaaaa 1807
254 <210> SEQ ID NO: 5
255 <211> LENGTH: 505
256 <212> TYPE: PRT
257 <213> ORGANISM: Limnanthes douglasii
259 <220> FEATURE:

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260 <221> NAME/KEY: UNSURE
261 <222> LOCATION: (74) /
263 <220> FEATURE:
264 <221> NAME/KEY: UNSURE
265 <222> LOCATION: (77) /
267 <220> FEATURE:
268 <221> NAME/KEY: UNSURE
269 <222> LOCATION: (114) /
271 <400> SEQUENCE: 5
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273 1 5 10 15
275 Thr Leu Pro Asp Leu Lys Leu Ser Ile Asn Leu Lys His Val Lys Leu
276 20 25 30
278 Gly Tyr His Tyr Leu Ile Thr His Gly Met Tyr Leu Cys Leu Pro Pro
279 35 40 45
281 Leu Ala Leu Val Leu Phe Ala Gln Ile Ser Thr Leu Ser Leu Lys Asp
282 50 55 60 /
W--> 284 Phe Asn Asp Ile Trp Glu Gln Leu Gln Xaa Asn Leu Xaa Ser Val Val
285 65 70 75 80
287 Val Ser Ser Thr Leu Val Ser Leu Leu Ile Leu Tyr Phe Met Thr
288 85 90 95
290 Arg Pro Arg Pro Val Tyr Leu Met Asp Phe Ala Cys Tyr Lys Pro Asp
291 / 100 105 110
W--> 293 Glu Xaa Arg Lys Ser Thr Arg Glu His Phe Met Lys Cys Gly Glu Ser
294 115 120 125
296 Leu Gly Ser Phe Thr Glu Asp Asn Ile Asp Phe Gln Arg Lys Leu Val
297 130 135 140
299 Ala Arg Ser Gly Leu Gly Asp Ala Thr Tyr Leu Pro Glu Ala Ile Gly
300 145 150 155 160
302 Thr Ile Pro Ala His Pro Ser Met Lys Ala Ala Arg Arg Glu Ala Glu
303 165 170 175
305 Leu Val Met Phe Gly Ala Ile Asp Gln Leu Leu Glu Lys Thr Lys Val
306 180 185 190
308 Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Cys Ser Leu Phe Ser
309 195 200 205
311 Pro Thr Pro Ser Leu Ser Ser Met Ile Val Asn His Tyr Lys Leu Arg
312 210 215 220
314 Gly Asn Ile Ile Ser Tyr Asn Leu Gly Gly Met Gly Cys Ser Ala Gly
315 225 230 235 240
317 Leu Ile Ser Val Asp Leu Ala Lys Arg Leu Leu Glu Thr Asn Pro Asn
318 245 250 255
320 Thr Tyr Ala Leu Val Met Ser Thr Glu Asn Ile Thr Leu Asn Trp Tyr
321 260 265 270
323 Met Gly Asn Asp Arg Ser Lys Leu Val Ser Asn Cys Leu Phe Arg Met
324 275 280 285
326 Gly Gly Ala Ala Val Leu Leu Ser Asn Lys Thr Ser Asp Lys Lys Arg
327 290 295 300
329 Ser Lys Tyr Gln Leu Val Thr Thr Val Arg Ser His Lys Gly Ala Asp
330 305 310 315 320

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VERIFICATION SUMMARY DATE: 09/26/2000
PATENT APPLICATION: US/09/664,840 TIME: 12:02:25

Input Set : A:\BB1117 US NA Seq Listing.txt
Output Set: N:\CRF3\09262000\I664840.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:227 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:227 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
L:229 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
M:340 Repeated in SeqNo=4
L:250 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:284 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:284 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:293 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
M:340 Repeated in SeqNo=5